AMENDMENT

Please amend the application without prejudice, without admission, without surrender of the subject matter, and without any intention of creating any estoppel as to equivalents as follows.

In the Specification

Please rewrite the paragraph beginning on page 16, line 15, as follows:

-- Due to the (endogenous) restriction sites present in a plant genome prior to incorporation of the foreign DNA, insertion of a foreign DNA will alter the specific restriction map of that genome. Thus, a particular transformant or progeny derived thereof can be identified by one or more specific restriction patterns. The conditions for determining the restriction map of an event are laid out in a "restriction map identification protocol". Alternatively, plants or plant material comprising an elite event can be identified by testing according to a PCR identification protocol. This is a PCR using primers that specifically recognize the elite event. Essentially, a set of primers is developed which recognizes a) a sequence within the 3' or 5' flanking sequence of the elite event and b) a sequence within the foreign DNA, which primers amplify a fragment (integration fragment) preferably of between 100 and 300 nucleotides. Preferably, a control is included of a set of primers that amplifies a fragment within a housekeeping gene of the plant species (preferably a fragment which is larger than the amplified integration fragment). ~~Oligonucleotides used as primers have different sequences and are complementary to sequences that (1) lie on opposite strands of the template DNA and (2) flank the segment of DNA that is to be amplified. Oligonucleotides used for priming the polymerase chain reaction should be at least 16 nucleotides, and preferably 20-24 nucleotides, in length.~~ The optimal conditions for the PCR, including the sequence of the specific primers are specified in a PCR identification protocol. --